



Db 361 EKLSRLAKLSGGVAVIKVATGATETELKEKRLIEDLALMTFRAVVEEDIVAGGTLANV 420  
Oy 421 IEKVALELEGDDATGRNIVLRALEBPVQIALNAGTSGSVIDKLKNSPAGTGFNAATG 480  
Db 421 IFAVATLELGDEATGRNIVLRALEBPVQIALNAGTSGSVIDKLKNSPAGTGFNAATG 480  
Oy 481 EVMNDIKTGIIIDPVKTSALONAAVASLITTEAVYANKPREPATPPAPAPAGNDGGM 540  
Db 481 EVMNDIKTGIIIDPVKTSALONAAVASLITTEAVYANKPREPATPPAPAPAGNDGGM 540  
Oy 541 GGM 543  
Db 537 GGM 539

## RESULT 2

Chapteronin GroEL (Imported) - Streptococcus pneumoniae (strain R6)  
C:Species: Streptococcus pneumoniae  
C:Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 02-Nov-2001  
C:Accession: H98086  
R:Authors: J.A.: Alborn Jr., W.: Arnold, J.: Blaszcak, L.: Burgelt, S.: Dehoff, B.S.: E  
y, R.: Leblanc, D.J.: Lee, L.N.: Lefkowitz, E.J.: Lu, J.: Matsushima, P.: Mchren, S.: M  
y, P.: Sun, P.M.: Winkler, M.E.  
J. Bacteriol. 183, 5709-5717, 2001  
A:Authors: Yang, Y.: Young-Bellido, M.: Zhao, G.: Zook, C.: Baltz, R.H.: Jaskunas, S.R.:  
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A:Reference number: A97872; MUID:21429245; PMID:11544234  
A:Accession: H98086  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-540 <CUR>  
A:Cross-references: GB:AE007317; PIDN:AA00025.1; PID:915459401; GSPDB:GN00174  
C:Genetics:  
A:Gene: groEL  
A:Superfamily: chaperonin groEL

Query Match 88.1%; Score 2347; DB 2; Length 540;  
Best Local Similarity 87.8%; Pred. No. 9.7e-110;  
Matches 477; Conservative 34; Mismatches 28; Indels 4; Gaps 1;

Oy 1 MAKEIKFSADARAANVRCVMDLADTVKVTLPGRGRNVLEKAFGSPPLITNDGVTIAKEIE 60  
Db 1 MSKEIKFSADARAANVRCVMDLADTVKVTLPGRGRNVLEKAFGSPPLITNDGVTIAKEIE 60  
Oy 61 LEDHEENNGAKLVSEVASKTNDIAGDGTATVLTQAIHVEGLKNTAGANPIGIRGIE 120  
Db 61 LEDHEENNGAKLVSEVASKTNDIAGDGTATVLTQAIHVEGLKNTAGANPIGIRGIE 120  
Oy 121 TATATVAELKAIAPVSGKEAIAOVAANSSRSKVEYISEAMERVCNGCVITTEESRG 180  
Db 121 TATATVAELKAIAPVSGKEAIAOVAANSSRSKVEYISEAMERVCNGCVITTEESRG 180  
Oy 181 METELEVENGKOPDRGTLISQYMTDNEKVADELNPFLITDKKVSINQIILPLEEVK 240  
Db 181 METELEVENGKOPDRGTLISQYMTDNEKVADELNPFLITDKKVSINQIILPLEEVK 240  
Oy 241 TNRPLLIADDDVGEALPTLVNKRIGTFNNVAVKAPGFGDRRKAMEIDAILTGTIVT 300  
Db 241 TNRPLLIADDDVGEALPTLVNKRIGTFNNVAVKAPGFGDRRKAMEIDAILTGTIVT 300  
Oy 301 EDGLLEKDATMTALGOAAKITVDKSTVIVEGSGSSSEAIANRIALIKISOLETTSPDR 360  
Db 301 EDGLLEKDATMTALGOAAKITVDKSTVIVEGSGSSSEAIANRIALIKISOLETTSPDR 360  
Oy 361 EKLOERLAKLAGVAVIKVAPETALKEKMLRIEDALNATRAAVEGIVAGGGTALTIV 420  
Db 361 EKLOERLAKLAGVAVIKVAPETALKEKMLRIEDALNATRAAVEGIVAGGGTALTIV 420  
Oy 421 IEKVALELEGDDATGRNIVLRALEBPVQIALNAGTSGSVIDKLKNSPAGTGFNAATG 480  
Db 421 IEKVALELEGDDATGRNIVLRALEBPVQIALNAGTSGSVIDKLKNSPAGTGFNAATG 480  
Oy 541 GGM 543  
Db 537 GGM 539

## RESULT 3

60 kb chaperonin (Imported) - Lactococcus lactis subsp. lactis (strain IL1403)  
C:Species: Lactococcus lactis subsp. lactis  
C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001  
C:Accession: B86674  
R:Authors: A.: Winkler, P.: Manger, S.: Jallion, O.: Malarme, K.: Welschenbach, J.: El  
Genome Res. 11, 731-753, 2001  
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis  
A:Reference number: A86625; MUID:21235186; PMID:11337471  
A:Accession: B86674  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-542 <STO>  
A:Cross-references: GB:AE005176; PID:912723267; PIDN:AA04492.1; GSPDB:GN00146  
A:Experimental source: strain IL1403  
C:Genetics:  
A:Gene: groEL  
A:Superfamily: chaperonin groEL

Query Match 82.4%; Score 2195.5; DB 2; Length 542;  
Best Local Similarity 81.1%; Pred. No. 3.4e-102;  
Matches 442; Conservative 52; Mismatches 46; Indels 5; Gaps 3;

Oy 1 MAKEIKFSADARAANVRCVMDLADTVKVTLPGRGRNVLEKAFGSPPLITNDGVTIAKEIE 60  
Db 1 MSKEIKFSADARAANVRCVMDLADTVKVTLPGRGRNVLEKAFGSPPLITNDGVTIAKEIE 60  
Oy 61 LEDHEENNGAKLVSEVASKTNDIAGDGTATVLTQAIHVEGLKNTAGANPIGIRGIE 120  
Db 61 LEDHEENNGAKLVSEVASKTNDIAGDGTATVLTQAIHVEGLKNTAGANPIGIRGIE 120  
Oy 121 TATATVAELKAIAPVSGKEAIAOVAANSSRSKVEYISEAMERVCNGCVITTEESRG 180  
Db 121 TATATVAELKAIAPVSGKEAIAOVAANSSRSKVEYISEAMERVCNGCVITTEESRG 180  
Oy 181 METELEVENGKOPDRGTLISQYMTDNEKVADELNPFLITDKKVSINQIILPLEEVK 240  
Db 181 METELEVENGKOPDRGTLISQYMTDNEKVADELNPFLITDKKVSINQIILPLEEVK 240  
Oy 241 TNRPLLIADDDVGEALPTLVNKRIGTFNNVAVKAPGFGDRRKAMEIDAILTGTIVT 300  
Db 241 TNRPLLIADDDVGEALPTLVNKRIGTFNNVAVKAPGFGDRRKAMEIDAILTGTIVT 300  
Oy 301 EDGLLEKDATMTALGOAAKITVDKSTVIVEGSGSSSEAIANRIALIKISOLETTSPDR 360  
Db 301 EDGLLEKDATMTALGOAAKITVDKSTVIVEGSGSSSEAIANRIALIKISOLETTSPDR 360  
Oy 361 EKLOERLAKLAGVAVIKVAPETALKEKMLRIEDALNATRAAVEGIVAGGGTALTIV 420  
Db 361 EKLOERLAKLAGVAVIKVAPETALKEKMLRIEDALNATRAAVEGIVAGGGTALTIV 420  
Oy 421 IEKVALELEGDDATGRNIVLRALEBPVQIALNAGTSGSVIDKLKNSPAGTGFNAATG 480  
Db 421 IEKVALELEGDDATGRNIVLRALEBPVQIALNAGTSGSVIDKLKNSPAGTGFNAATG 480  
Oy 481 EVMNDIKTGIIIDPVKTSALONAAVASLITTEAVYANKPREPATPPAPAPAGNDGGM 540  
Db 481 EVMNDIKTGIIIDPVKTSALONAAVASLITTEAVYANKPREPATPPAPAPAGNDGGM 540  
Oy 541 GGM 543  
Db 537 GGM 539

## RESULT 4

JN0661  
 heat shock protein groEL - Lactococcus lactis subsp. lactis  
 C:Species: Lactococcus lactis subsp. lactis  
 C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 17-Mar-1999  
 C:Accession: JN0661  
 R:Klim S.G., Batt, C.A.  
 Gene 127, 121-126, 1993  
 A:Title: Cloning and sequencing of Lactococcus lactis subsp. lactis groEL operon.  
 A:Reference number: JN0660; M0ID:93252268; PMID:8486277  
 A:Accession: JN0661  
 A:Molecule type: DNA  
 A:Residues: 1-542 <KIM>  
 C:Genetics:  
 A:Gene: groEL  
 C:Superfamily: chaperonin groEL  
 C:Keywords: heat shock; molecular chaperone; stress-induced protein

Query Match 81.5%; Score 2171.5; DB 2; Length 542;  
 Best Local Similarity 80.4%; Pred. No. 5.3e-101;  
 Matches 438; Conservative 53; Mismatches 49; Indels 5; Gaps 3;

OY 1 MAKEIFSDARAAVRGVDMADTVKVTIGPKRNVYLEKAFSGPLITNDGVTIAKEIE 60  
 DB 1 MSKDIKFSDDARTAMRGIDILADTVKTTIGPKRNVYLEKSGPLITNDGVTIAKEIE 60  
 OY 61 LEHFENMGAKLVSEVASKTNDIAGDGTATVLTQAIHVEGLKNTAGANPVGIRGIE 120  
 DB 61 LEHFENMGAKLVSEVASKTNDIAGDGTATVLTQAIHVEGLKNTAGANPVGIRGIE 120  
 OY 121 TATATAVEALKAIAPVSGKEALIAQVAVSSRSSEKVEYISEAMERVNDGVITIEESRG 180  
 DB 121 LAETVAVASIKEMAIPIVHDKSAIAQVAVSSRSSEKVEYISDAMERVNDGVITIEESRG 180  
 OY 181 METELEVEGMOFDRGYLSQYVWTDNEKVAADLENPILITDKKVSNIQDILPLEEVLK 240  
 DB 181 MOTELDVEGMOFDRGYLSQYVWTDNEKVAADLENPILITDKKVSNIQDILPLEEVLK 240  
 OY 241 TNRPLLIADVDGEALPTVLNKRIGTFENVVAKPFGDGRKAKOLEHAILTGCTVIT 300  
 DB 241 TNRPLLIADVDGEALPTVLNKRIGTFENVVAKPFGDGRKAKOLEHAILTGCTVIT 300  
 OY 301 EDLGLKDATMTALGOAAKITVDKSTVIEGSSSEAIAMRIALIKSOLETTSDPR 360  
 DB 301 BELGDLKDATLEALGOAAKITVDKSTVIEGSSSEAIAMRIALIKSOLETTSDPR 360  
 OY 361 EKLOERLAKIAGVAVIKVGAFTETALKEKRIEDALNATRAVEGIVAGGATLTV 420  
 DB 361 EKLOERLAKIAGVAVIKVGAFTETALKEKRIEDALNATRAVEGIVAGGATLTV 420  
 OY 421 IEKVALELEGGDATGRNIVLRALPEVRQIALNAGVEGIVIDKLNSPAGTGFNAATG 480  
 DB 421 IALDKLSEESDITQIGINIVRRALPEVRQIALNAGVEGIVIDKLNSPAGTGFNAATG 480  
 OY 481 EYVDMIKTGIIIDPVKVTASALONAAVSLITTEAVVANKPEPATPAPAMPAGMDPGM 540  
 DB 481 QVNMIEEGIVDPKAVTASALONAAVSLITTEAVVANKPEPATPAPAMPAGMDPGM 540  
 OY 541 GGMGG 545  
 DB 537 -GMSG 540

## RESULT 5

S32106  
 groEL protein - Lactococcus lactis  
 C:Species: Lactococcus lactis  
 C:Date: 06-Jan-1993 #sequence\_revision 06-Jan-1995 #text\_change 26-Aug-1999  
 C:Accession: S32106  
 R:Batt, C.A.  
 Submitted to the EMBL Data Library, March 1993

A:Reference number: S32105  
 A:Accession: S32106  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-542 <BAT>  
 A:Cross-references: EMBL:X71132; NID:g287869; PID:CAA50446.1; PID:g287871  
 C:Superfamily: chaperonin groEL

Query Match 81.5%; Score 2171.5; DB 2; Length 542;  
 Best Local Similarity 80.4%; Pred. No. 5.3e-101;  
 Matches 438; Conservative 53; Mismatches 49; Indels 5; Gaps 3;

OY 1 MAKEIFSDARAAVRGVDMADTVKVTIGPKRNVYLEKAFSGPLITNDGVTIAKEIE 60  
 DB 1 MSKDIKFSDDARTAMRGIDILADTVKTTIGPKRNVYLEKSGPLITNDGVTIAKEIE 60  
 OY 61 LEHFENMGAKLVSEVASKTNDIAGDGTATVLTQAIHVEGLKNTAGANPVGIRGIE 120  
 DB 61 LEHFENMGAKLVSEVASKTNDIAGDGTATVLTQAIHVEGLKNTAGANPVGIRGIE 120  
 OY 121 TATATAVEALKAIAPVSGKEALIAQVAVSSRSSEKVEYISEAMERVNDGVITIEESRG 180  
 DB 121 LAETVAVASIKEMAIPIVHDKSAIAQVAVSSRSSEKVEYISDAMERVNDGVITIEESRG 180  
 OY 181 METELEVEGMOFDRGYLSQYVWTDNEKVAADLENPILITDKKVSNIQDILPLEEVLK 240  
 DB 181 MOTELDVEGMOFDRGYLSQYVWTDNEKVAADLENPILITDKKVSNIQDILPLEEVLK 240  
 OY 241 TNRPLLIADVDGEALPTVLNKRIGTFENVVAKPFGDGRKAKOLEHAILTGCTVIT 300  
 DB 241 TNRPLLIADVDGEALPTVLNKRIGTFENVVAKPFGDGRKAKOLEHAILTGCTVIT 300  
 OY 301 EDLGLKDATMTALGOAAKITVDKSTVIEGSSSEAIAMRIALIKSOLETTSDPR 360  
 DB 301 BELGDLKDATLEALGOAAKITVDKSTVIEGSSSEAIAMRIALIKSOLETTSDPR 360  
 OY 361 EKLOERLAKIAGVAVIKVGAFTETALKEKRIEDALNATRAVEGIVAGGATLTV 420  
 DB 361 EKLOERLAKIAGVAVIKVGAFTETALKEKRIEDALNATRAVEGIVAGGATLTV 420  
 OY 421 IEKVALELEGGDATGRNIVLRALPEVRQIALNAGVEGIVIDKLNSPAGTGFNAATG 480  
 DB 421 IALDKLSEESDITQIGINIVRRALPEVRQIALNAGVEGIVIDKLNSPAGTGFNAATG 480  
 OY 481 EYVDMIKTGIIIDPVKVTASALONAAVSLITTEAVVANKPEPATPAPAMPAGMDPGM 540  
 DB 481 QVNMIEEGIVDPKAVTASALONAAVSLITTEAVVANKPEPATPAPAMPAGMDPGM 540  
 OY 541 GGMGG 545  
 DB 537 -GMSG 540

## RESULT 6

AD1333  
 class I heat-shock protein (chaperonin) GroEL (imported) - Listeria monocytogenes  
 C:Species: Listeria monocytogenes  
 C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 14-Dec-2001  
 C:Accession: AD1333  
 R:Glaser, P.; Frangoul, L.; Buchteser, C.; Amend, A.; Baquero, F.; Berche, P.; B.  
 D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlian, K.D.; F.  
 J.; Jones, L.M.; Karsic, U.  
 Science 294, 849-852, 2001  
 A:Authors: Krefte, J.; Kuhn, M.; Kunst, F.; Kurpkat, G.; Madueno, E.; Maltournam,  
 O.K.; C.; Schueter, T.; Simoes, N.; Tietze, A.; Vazquez-Boland, J.A.; Voss, H.; W.  
 A:Title: Comparative genomics of Listeria species.  
 A:Reference number: AB1077; M0ID:21537279; PMID:11679669  
 A:Accession: AD1333  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-542 <GLA>  
 A:Cross-references: GB:NC\_003210; PID:CAD00146.1; PID:g16411538; GSPDB:GM00177  
 A:Experimental source: strain EGo-e

C:Genetics:  
A:Gene: groEL  
C:Superfamily: Chaperonin groEL

Query Match 76.4%; Score 2033.5; DB 2; Length 542;  
Best Local Similarity 75.6%; Pred. No. 3.9e-94;  
Matches 412; Conservative 61; Mismatches 67; Indels 5; Gaps 3;

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Oy 1 MAKEIKESADARAAAMRGVMDLADYVKTGLPGKRNVLLEKAFSPILITNDGVTIAKEIE 60
    |||:||||| ||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 1 MAKDIKESADARAAAMRGVMDLADYVKTGLPGKRNVLLEKAFSPILITNDGVTIAKEIE 60
Oy 61 LEDPENNAGALVSEVASTNDVAGDGTATATVLAQMIHGEUKNTAGANVGVGRIE 120
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 61 LEDPENNAGALVSEVASTNDVAGDGTATATVLAQMIHGEUKNTAGANVGVGRIE 120
Oy 121 TATATVPEALKAIAQPVSGKEAIAQVAASVSEKVEYISEAMERVNDGVITIEESRG 180
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 121 KAAVATLIEELKAISKPIESKESIAQVAASVSEKVEYISEAMERVNDGVITIEESRG 180
Oy 181 METELEVEGMOFDRGYLSQVNTDNEKNVADLENPFILITDKKVSNTODILPLEEVK 240
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 181 FATELDVVEGMOFDRGYTSPTVNTDSKMEAVLEKPYILITDKKINNIOELIVLEQVVO 240
Oy 241 TNRPLLIADVDGEALPTLVNKRIGTFNNVAVKAPGDRRKAMLEDAIILTGCVIT 300
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 241 OGRPLLIADVEGEAQAATLVNKRIGTFNNVAVKAPGDRRKAMLEDAIILTGCVIT 300
Oy 301 EDLGELEKATVDTALGOAAKITVDKSTVIEGSSSEAIANRIALIKSOLETTTSPDR 360
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 301 EDLGELEKATVDTALGOAAKITVDKSTVIEGSSSEAIANRIALIKSOLETTTSEPR 360
Oy 361 EKLOERLAKLAGVAIVKAPETALKEKRLIEDALNTRAIVEGIVAGGTAITV 420
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 361 EKLOERLAKLAGVAIVKAPETALKEKRLIEDALNTRAIVEGIVAGGTAITV 420
Oy 421 IEKVALELEDGDATGRNIVRALPEPVROIALNAGIEGVIDIKKSPAGTGFNAATG 480
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 421 YKKVALELEDGDATGRNIVRALPEPVROIALNAGIEGVIDIKKSPAGTGFNAAG 480
Oy 481 EWDNMTKIGIIDPVKVTTSALONAAVASLITTEAVVANKPEPATPAPAMAGDPGM 540
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 481 EWNMTMDAGIVDPKVTTSALONAAVASLITTEAVVADKPENGA- - -AGDMG- -M 535
Oy 541 GGMCG 545
    |||:|||||
Db 536 GGMCG 540

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## RESULT 7

AC1104  
C:Species: *Listeria innocua* (chaperonin) GroEL (imported) - *Listeria innocua* (strain Clif  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 14-Dec-2001  
C:Accession: AC1104  
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker  
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlian, K.D.; Fsihl, H.  
D.; Jones, L.M.; Karet, U.  
Science 294, 849-852, 2001  
A:Authors: Krett, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madheno, E.; Maltournam, A.; Ma  
ok, C.; Schlueter, T.; Simoes, N.; Tietz, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,  
A:Title: Comparative genomics of *Listeria* species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AC1104  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-542 <GLA>  
A:Cross-references: GB:AL592023; PIDN:CMC97403.1; PID:q16414687, GSPDB:GN00178  
A:Experimental source: strain Clif11262  
C:Genes: groEL  
C:Superfamily: chaperonin groEL

Query Match 76.1%; Score 2026.5; DB 2; Length 542;  
Best Local Similarity 75.0%; Pred. No. 8.8e-94;  
Matches 409; Conservative 62; Mismatches 69; Indels 5; Gaps 2;

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Oy 1 MAKEIKESADARAAAMRGVMDLADYVKTGLPGKRNVLLEKAFSPILITNDGVTIAKEIE 60
    |||:||||| ||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 1 MAKDIKESADARAAAMRGVMDLADYVKTGLPGKRNVLLEKAFSPILITNDGVTIAKEIE 60
Oy 61 LEDPENNAGALVSEVASTNDVAGDGTATATVLAQMIHGEUKNTAGANVGVGRIE 120
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 61 LEDPENNAGALVSEVASTNDVAGDGTATATVLAQMIHGEUKNTAGANVGVGRIE 120
Oy 121 TATATVPEALKAIAQPVSGKEAIAQVAASVSEKVEYISEAMERVNDGVITIEESRG 180
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 121 KAAVATLIEELKAISKPIESKESIAQVAASVSEKVEYISEAMERVNDGVITIEESRG 180
Oy 181 METELEVEGMOFDRGYLSQVNTDNEKNVADLENPFILITDKKVSNTODILPLEEVK 240
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 181 FATELDVVEGMOFDRGYTSPTVNTDSKMEAVLEKPYILITDKKINNIOELIVLEQVVO 240
Oy 241 TNRPLLIADVDGEALPTLVNKRIGTFNNVAVKAPGDRRKAMLEDAIILTGCVIT 300
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 241 OGRPLLIADVEGEAQAATLVNKRIGTFNNVAVKAPGDRRKAMLEDAIILTGCVIT 300
Oy 301 EDLGELEKATVDTALGOAAKITVDKSTVIEGSSSEAIANRIALIKSOLETTTSPDR 360
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 301 EDLGELEKATVDTALGOAAKITVDKSTVIEGSSSEAIANRIALIKSOLETTTSEPR 360
Oy 361 EKLOERLAKLAGVAIVKAPETALKEKRLIEDALNTRAIVEGIVAGGTAITV 420
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 361 EKLOERLAKLAGVAIVKAPETALKEKRLIEDALNTRAIVEGIVAGGTAITV 420
Oy 421 IEKVALELEDGDATGRNIVRALPEPVROIALNAGIEGVIDIKKSPAGTGFNAATG 480
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 421 YKKVALELEDGDATGRNIVRALPEPVROIALNAGIEGVIDIKKSPAGTGFNAAG 480
Oy 481 EWDNMTKIGIIDPVKVTTSALONAAVASLITTEAVVANKPEPATPAPAMAGDPGM 540
    |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 481 EWNMTMDAGIVDPKVTTSALONAAVASLITTEAVVADKPENGA- - -AGDMG- -M 535
Oy 541 GGMCG 545
    |||:|||||
Db 536 GGMCG 540

```

## RESULT 8

B41884  
58k heat shock protein groEL - *Bacillus subtilis*  
N:Alternate names: class I heat-shock protein (chaperonin) groEL  
C:Species: *Bacillus subtilis*  
C:Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 20-Jun-2000  
C:Accession: B41884; B41885; J01372; B47683; D69637  
R:Li, M.; Wong, S.L.  
J. Bacteriol. 174, 3981-3992, 1992  
A:Title: Cloning and characterization of the groESL operon from *Bacillus subtilis*.  
A:Reference number: A41884; MUID:92283753; PMID:1350776  
A:Accession: B41884  
A:Molecule type: DNA  
A:Residues: 1-544 <LI>  
A:Cross-references: GB:M1132; NID:q143025; PIDN:AAA2503.1; PID:q143027  
A:Experimental source: strain 168  
A:Note: Sequence extracted from NCBI backbone (NCBIN:105982, NCBI:P.105989)  
R:Schmidt, A.; Schlesswohl, M.; Volker, U.; Hecker, M.; Schumann, W.  
J. Bacteriol. 174, 3993-3999, 1992  
A:Title: Cloning, sequencing, mapping, and transcriptional analysis of the groESL op  
A:Reference number: A41885; MUID:92283754; PMID:1350777  
A:Accession: B41885  
A:Molecule type: DNA  
A:Residues: 1-544 <SCH>  
A:Cross-references: GB:M84965; NID:q143061; PIDN:AAA22531.1; PID:q143063  
A:Experimental source: strain MB1  
A:Note: Sequence extracted from NCBI backbone (NCBIN:105432, NCBI:P.105434)  
R:Itazawa, Y.; Yoshikawa, H.; Kawamura, F.; Itaya, M.; Takahashi, H.

Biosci. Biotechnol. Biochem. 56, 1995-2002, 1992  
 A:Title: Isolation and characterization of the groES and groEL genes of *Bacillus subtilis*  
 A:Reference number: JCI371; MUID:93129852; PMID:1369494  
 A:Accession: JCI372  
 A:Molecule type: DNA  
 A:Residues: 1-14, 'N', 16-124, 'L', 126-201, 'L', 203-374, 'R', 376-544 <TO2>  
 A:Cross-references: GB:ID0972; GB:ID01157; NID:94433779; PIDN:BA22519.1; PID:94433781  
 A:Experimental source: strain Marburg 168  
 A:Note: the authors translated the codon AAT for residue 15 as Met  
 J. Volker, U. Mach, H. Schmid, R. Becker, M.  
 J. Gen. Microbiol. 138, 2125-2135, 1992  
 A:Title: Stress proteins and cross-protection by heat shock and salt stress in *Bacillus*  
 A:Reference number: A47683; MUID:93123969; PMID:1362210  
 A:Contents: IS58  
 A:Accession: B47683  
 A:Molecule type: protein  
 A:Residues: 2-31 <VOL>  
 A:Note: sequence extracted from NCBI backbone (NCBI:121871)  
 R. Kunst, F. Ogasawara, N. Moszer, I. Altshuler, A. M. Alloni, G. Azevedo, V. Bertet, C. Bron, S. Brouillet, S. Bruch, C. V. Caldwell, B. Capuano, V. Carter, N. M. Cho, Nature 390, 249-256, 1997  
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizel, A.; Gallier, J.; Harwood, C. R.; Henaut, A.; Hiltbert, R.; Holtsappel, S.; Hosono, S.; Hullo, M. F.; Koeltter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, Y. M.; Ogawa, K.; Ogawa, A.; Oudega, B.; Park, S. H.; Parro, V.; Pohl, T. M.; Portet, R.; Rieger, M.; Rivolta, C.; Roche, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, A.; Schuster, S.; Schuster, R.; Scott, R.; Scott, F.; Sekiguchi, J.; Sekowska, A.; Serot, A.; Whithers, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.  
 A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.  
 A:Reference number: A69580; MUID:98044033; PMID:9384377  
 A:Accession: D69637  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-544 <UN>  
 A:Cross-references: GB:299107; GB:AL009126; NID:92632866; PIDN:CA12422.1; PID:92632916  
 A:Experimental source: strain 168  
 A:Genetic: groEL  
 A:Gene: groEL  
 C:Superfamily: chaperonin groEL  
 C:Keywords: heat shock; molecular chaperone; stress-induced protein

Query Match 75.18; Score 2026.5; DB 2; Length 544;  
 Best Local Similarity 73.84; Pred. No. 8; 8e-94;  
 Matches 402; Conservative 69; Mismatches 71; Indels 3; Gaps 1;

OY 1 MAKEIKFSADARAANVGVMDLADYKVTLPKGRNVLEKAFSGPLITNDGVTIAKEIE 60  
 DB 1 MAKEIKFSADARAANVGVMDLADYKVTLPKGRNVLEKAFSGPLITNDGVTIAKEIE 60  
 OY 61 LEDHFENMGAKLVEVASKTNDIAGDGTATVLTQAIHVEGLKNTAGANPGRIGIE 120  
 DB 61 LEDHFENMGAKLVEVASKTNDIAGDGTATVLTQAIHVEGLKNTAGANPGRIGIE 120  
 OY 121 TATATAVEALKAIAPVSGKEAIAOVAASRSRSEKVEYSSEAMRVNGDGVITIEERG 180  
 DB 121 TATATAVEALKAIAPVSGKEAIAOVAASRSRSEKVEYSSEAMRVNGDGVITIEERG 180  
 OY 181 MEPELEVEGMOFGRGLSYMTDNEKVAADLENPILITDKKSNIDILPLEEYK 240  
 DB 181 MEPELEVEGMOFGRGLSYMTDNEKVAADLENPILITDKKSNIDILPLEEYK 240  
 OY 241 TNRPLITADVDGEALPTLVNKRIGTFNVAVAKPGFDRRKAMLEDAITLGTGVT 300  
 DB 241 TNRPLITADVDGEALPTLVNKRIGTFNVAVAKPGFDRRKAMLEDAITLGTGVT 300  
 OY 301 EDGLLEKDATMTALGOAANKITVDKSTVIEGSSSEAIANRIALIKSOLETTSDPR 360  
 DB 301 EDGLLEKDATMTALGOAANKITVDKSTVIEGSSSEAIANRIALIKSOLETTSDPR 360  
 OY 481 EYMDIKGTGIIDPKVTRSAIOMASVASLITTEVYANPEEPATPAPAMAGNDGGM 540  
 DB 481 EYMDIKGTGIIDPKVTRSAIOMASVASLITTEVYANPEEPATPAPAMAGNDGGM 540  
 OY 541 GGMG 545  
 DB 541 GGMG 545

361 EKLOERLAKLAGVAIVKGAFTETALKENKRIEDALNATRAAEEGIVAGGTALITV 420  
 DB 361 EKLOERLAKLAGVAIVKGAFTETALKENKRIEDALNATRAAEEGIVAGGTALITV 420  
 OY 421 IEKVALELEDGDAATGRNIVLRALEPEPYROTALNAGCEGIVADKNSPAGTGNATG 480  
 DB 421 YNKVAAVEEGDAQTGINIVLRALEPEPIROTALNAGCEGIVADKNSPAGTGNATG 480  
 OY 481 EYMDIKGTGIIDPKVTRSAIOMASVASLITTEVYANPEEPATPAPAMAGNDGGM 540  
 DB 481 EYMDIKGTGIIDPKVTRSAIOMASVASLITTEVYANPEEPATPAPAMAGNDGGM 540  
 OY 541 GGMG 545  
 DB 541 GGMG 545

RESULT 9  
 B49855  
 heat shock protein GroEL - *Bacillus stearothermophilus*  
 C:Species: *Bacillus stearothermophilus*  
 C:Date: 07-Apr-1994 #sequence\_revision 18-Nov-1994 #text\_change 12-Sep-1997  
 A:Accession: B49855  
 R. Schon, U. Schumann, M.  
 J. Bacteriol. 175, 2465-2469, 1993  
 A:Title: Molecular cloning, sequencing, and transcriptional analysis of the groESL  
 A:Reference number: A49855; MUID:93224474; PMID:8096841  
 A:Accession: B49855  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-539 <SCH>  
 A:Note: sequence inconsistent with nucleotide translation  
 A:Note: sequence extracted from NCBI backbone (NCBI:129322, NCBI:129324)  
 C:Superfamily: chaperonin groEL

Query Match 75.98; Score 2021.5; DB 2; Length 539;  
 Best Local Similarity 74.98; Pred. No. 1; 1e-93;  
 Matches 408; Conservative 63; Mismatches 65; Indels 9; Gaps 2;

OY 1 MAKEIKFSADARAANVGVMDLADYKVTLPKGRNVLEKAFSGPLITNDGVTIAKEIE 60  
 DB 1 MAKEIKFSADARAANVGVMDLADYKVTLPKGRNVLEKAFSGPLITNDGVTIAKEIE 60  
 OY 61 LEDHFENMGAKLVEVASKTNDIAGDGTATVLTQAIHVEGLKNTAGANPGRIGIE 120  
 DB 61 LEDHFENMGAKLVEVASKTNDIAGDGTATVLTQAIHVEGLKNTAGANPGRIGIE 120  
 OY 121 TATATAVEALKAIAPVSGKEAIAOVAASRSRSEKVEYSSEAMRVNGDGVITIEERG 180  
 DB 121 KAVAAVEALKAIAPVSGKEAIAOVAASRSRSEKVEYSSEAMRVNGDGVITIEERG 180  
 OY 181 MEPELEVEGMOFGRGLSYMTDNEKVAADLENPILITDKKSNIDILPLEEYK 240  
 DB 181 FATELDVEGMOFGRGLSYMTDNEKVAADLENPILITDKKSNIDILPLEEYK 240  
 OY 241 TNRPLITADVDGEALPTLVNKRIGTFNVAVAKPGFDRRKAMLEDAITLGTGVT 300  
 DB 241 TNRPLITADVDGEALPTLVNKRIGTFNVAVAKPGFDRRKAMLEDAITLGTGVT 300  
 OY 301 EDGLLEKDATMTALGOAANKITVDKSTVIEGSSSEAIANRIALIKSOLETTSDPR 360  
 DB 301 EDGLLEKDATMTALGOAANKITVDKSTVIEGSSSEAIANRIALIKSOLETTSDPR 360  
 OY 361 EKLOERLAKLAGVAIVKGAFTETALKENKRIEDALNATRAAEEGIVAGGTALITV 420  
 DB 361 EKLOERLAKLAGVAIVKGAFTETALKENKRIEDALNATRAAEEGIVAGGTALITV 420  
 OY 421 IEKVALELEDGDAATGRNIVLRALEPEPYROTALNAGCEGIVADKNSPAGTGNATG 480  
 DB 421 YNKVAAVEEGDAQTGINIVLRALEPEPIROTALNAGCEGIVADKNSPAGTGNATG 480  
 OY 481 EYMDIKGTGIIDPKVTRSAIOMASVASLITTEVYANPEEPATPAPAMAGNDGGM 540  
 DB 481 EYMDIKGTGIIDPKVTRSAIOMASVASLITTEVYANPEEPATPAPAMAGNDGGM 540

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Db      481 EWMDINENAGIVDPKRYTSALQNNASVAANFLUTRAVYAAKPRE-----NKGNGPMP 533
OY      540 -MGCM 543
        |||||
Db      534 DMGGM 538

RESULT 10
JC6063
Chaperonin groEL - Bacillus sp.
C:Species: Bacillus sp.
C:Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 13-Sep-1998
C:Accession: JC6063
R:Xu, Y.; Zhou, P.-J.
Acta Microbiol. Sin. 36, 241-249, 1996
A:Title: Phylogeny of molecular chaperone 60 proteins.
A:Reference number: JC6063
A:Molecule type: DNA
A:Residues: 1-544 <XUA>
A:Experimental source: C-125 strain BD224
C:Genetics:
A:Gene: groEL
C:Superfamily: Chaperonin groEL
C:Keywords: molecular chaperone

Query Match          75.8% Score 2017.5: DB 2: Length 544;
Best Local Similarity 73.4%: Pred. No. 2.5e-93;
Matches 400: Conservative 74; Mismatches 68; Indels 3; Gaps 1

OY      1 MAKEKFSADRAARMRGMDLADYAVYLGRGRNVLEKAFSPGLTNDGTYTAKKE 60
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MKDKIFSDEARRSMKRGCDLADAKYVLGKGRNVYLEKAFSPGLTNDGTYTAKKE 60
OY      61 LEDHEENMGAKLVEASTNDIAGDGTTRATVLTQVYHEGLKNTVAGANPIGRGIE 120
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      61 LEDAEENMGAKLVAEYASTNDIAGDGTTRATVLTQVYHEGLKNTVAGANPIGRGIE 120
OY      121 TATATNVAELAKIAPVSGKEALIVQNAVSSRSKVEGYTISEMERGNDGVITIEESRG 180
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      121 KATQVAABELSKIPTEKDSIQAQVAISSADEVKKIIAEMERGNDSGVITIEESRG 180
OY      181 METELEVEGMOFDRGYLSQYMTVDEKKVADLENPFILITDKKXSNIDILPLEEYVK 240
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      181 FSTEELEVEGMOFDRGYLSQYMTVDEKKVADLENPFILITDKKXSNIDILPLEEYVK 240
OY      241 TNRPLLIADVDGEALPTLVLRKIRGFNFVNAVAKAAGFGDSRRKMLIEDAIIYTGATV 300
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      241 GQRPLLIADVDGEALPTLVLRKIRGFNFVNAVAKAAGFGDSRRKMLIEDAIIYTGATV 300
OY      301 EDLGLLEKLDATMTALGQAAKITVDKSDTYIEGSGSSEAIARIALITKSOLETTSSDPDR 360
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      301 EDLGLGDKTSANITQIGRASKVVYTKENTTYIEGAGSEDKIAARVQIKQAEETTSDEDK 360
OY      361 EKLDERLAKLAGVAVIVKYGAPETALKEMLRITEDALNTPRAAVEGYIAGGGTALTIV 420
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      361 EKLDERLAKLAGVAVIVKYGAAETEMKERLRITEDALNTPRAAVEGYIAGGGTALTIV 420
OY      421 IETKVALEKGGDPTAGRNIVRLALEEPYQALAGDESSVYIKLKNASPTAGGNATG 480
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      421 IKAVSSIGAGSDPTAGRNIVRLALEEPYQALAGDESSVYVERLKEELAGGEGNATG 480
OY      481 EAVMDITGIIQYVPTSSAALQAAVSAVSLITTEAVYANKEEPATPAAMPAGNDPQGM 540
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      481 EAVMNVAGIVDPKRYTSALQNNASVAANFLUTRAVYAAKPRE-----DMGGM 537
OY      541 GCMGCM 545
        |||||
Db      538 GCMGCM 542

RESULT 11
883720

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[illegible]

A:Reference number: J01194; MUID:91354309; PMID:16792330  
A:Accession: J01195  
A:Molecule type: DNA  
A:Residues: 1-538 <TAM>  
A:Note: part of this sequence, including both the amino and carboxyl ends of the mature  
A:Note: the nucleotide sequence encoding residues 531-538 is not shown in this paper  
R:Ohta, T.; Honda, K.; Saito, K.; Hayashi, H.; Tano, H.; Hamamoto, T.; Kagawa, Y.  
B:Ochem, Biophys. Res. Commun. 191, 550-557, 1993  
A:Title: Heat shock promoter of thermophilic chaperonin operon.  
A:Reference number: J01479; MUID:93213292; PMID:809682  
A:Accession: P01252  
A:Molecule type: DNA  
A:Residues: 1-79 <OHT>  
C:Comment: This protein is essential for the formation and restoration of many supramole  
C:Superfamily: chaperonin groEL  
C:Keywords: heat shock; stress-induced protein

A:Gene: groEL  
C:Superfamily: chaperonin groEL

Query Match 71.5%; Score 1905; Db 2; Length 538;  
Best Local Similarity 69.8%; Pred. No. 9,7e-88;

Matches 377; Conservative 78; Mismatches 83; Indels 2; Gaps 2;

```

QY 1 MAKIKFSADAAAVRGVMDLADVTYTLGPKRRNVLEKFPSPITIDGVTIAKIE 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MYKOLKESDARQALRGVDOQLANAVKVTIGPKRRNVLDKEFTAPLITIDGVTIAKIE 60
QY 61 LEDHFENMGAKLYSEVASKTNDIAGDGTATVTLQAIYHEGLKNVTAGANPIRGIE 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 LEDPYENMGAKLYQEVANKTNEIADGTTTATVLAQAMIOEGLKNVTSGANPVGLRGID 120
QY 121 TATATVAVALKAIAPVSGKEALIAOVAVSSRSSEKVGYSIEMERNGDCVITIEESRG 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 KAVKVAVALHENSCKVENKNEIQAQVISADEEIGRTISAEKVGNDGVITIEESRG 180
QY 161 METFELEVCGMOPDRGYLSQYNTYDNEKNVADLENPIILITDKKVSNIODILPLEEYVK 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 161 LNTLELEVCGMOPDRGYLSQYNTYDNEKNVADLENPIILITDKKVSNIODILPLEEYVK 240
QY 241 TNRPLLIADVDGALPTLVLNKIRGTFFNVVAVKAPGFGRRKAMLEDIAIILTGQVIT 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 241 SNRPILIVADEEGDALTNIVLNMRGTFAVAVKAPGFGRRKAMLEDIAIILTGQVIT 300
QY 301 EDLGLLELKDATMTALGQAATVVDKSTVIEGSGSSSEAIANRIALIKSQLETTSDPDR 360
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 301 DDLGLLKLKASIDMLGTASKVEYTKDNTVVDGDDENSIDARVSQLSQIEETSDPDR 360
QY 361 EKLOERLAKLAGVAVIKVGAFTETALKEKMLRIEDALNATRAVEGSIYAGGTAITLV 420
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 361 EKLOERLAKLAGVAVIKVGAFTETALKEKMLRIEDALNATRAVEGSIYAGGTAITLV 420
QY 421 IERVAALELEDGATGRNIVLRALPEPVROIALNAGVSVYIDLKNSPAGTGPNATG 480
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 421 YQKVSIELEEDDIETGVNIYKALTAAPVQIAENAGLEGSIVYERLKNAPGVGNATIN 480
QY 481 EPMYDMKTIIDIPVKVTRSAALONAAVASLITTEVAANKPEPATPAMPAGMDPGM 540
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 481 EPMYDMKTIIDIPVKVTRSAALONAAVASLITTEVAANKPEPATPAMPAGMDPGM 540

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# RESULT 15

JN0601  
heat shock protein 60 - Staphylococcus aureus  
C:Species: Staphylococcus aureus  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 12-Sep-1997  
C:Accession: JN0601; P05008  
R:Ohta, T.; Honda, K.; Kuroda, M.; Saito, K.; Hayashi, H.  
Biochem. Biophys. Res. Commun. 193, 730-737, 1993  
A:Title: Molecular characterization of the gene operon of heat shock proteins HSP60 and  
A:Reference number: JN0600; M01D:93290669; PMID:7916607  
A:Accession: JN0601  
A:Molecule type: DNA  
A:Residues: 1-539 <OH1>  
A:Accession: P05008  
A:Molecule type: Protein  
A:Residues: 1-21 <OH2>  
C:Genetics:  
A:Gene: hsp60  
C:Superfamily: chaperonin groEL  
C:Keywords: heat shock; stress-induced protein

Query Match 69.4%; Score 1847.5; Db 2; Length 539;  
Best Local Similarity 68.3%; Pred. No. 7.1e-85;  
Matches 371; Conservative 78; Mismatches 87; Indels 7; Gaps 4;

```

QY 1 MAKEIFSDARAAVAVRGVMDLADVTYTLGPKRRNVLEKFPSPITIDGVTIAKIE 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MYKOLKESDARQALRGVDOQLANAVKVTIGPKRRNVLDKEFTAPLITIDGVTIAKIE 60

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QY 61 LEDHFENMGAKLYSEVASKTNDIAGDGTATVTLQAIYHEGLKNVTAGANPIRGIE 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 LEDPYENMGAKLYQEVANKTNEIADGTTTATVLAQAMIOEGLKNVTSGANPVGLRGID 120
QY 121 TATATVAVALKAIAPVSGKEALIAOVAVSSRSSEKVGYSIEMERNGDCVITIEESRG 177
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 KAVKVAVALHENSCKVENKNEIQAQVISADEEIGRTISAEKVGNDGVITIEESRG 180
QY 178 SGMCTELEVEBGMOPDRGYLSQYNTYDNEKNVADLENPIILITDKKVSNIODILPLEEYVK 237
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 181 SNRPILIVADEEGDALTNIVLNMRGTFAVAVKAPGFGRRKAMLEDIAIILTGQVIT 238
QY 238 VLKTRPLLIADVDGALPTLVLNKIRGTFFNVVAVKAPGFGRRKAMLEDIAIILTGQVIT 297
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 238 VLKTRPLLIADVDGALPTLVLNKIRGTFFNVVAVKAPGFGRRKAMLEDIAIILTGQVIT 298
QY 298 VTEBDLGLLELKDATMTALGQAATVVDKSTVIEGSGSSSEAIANRIALIKSQLETTSDPDR 357
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 298 VTEBDLGLLELKDATMTALGQAATVVDKSTVIEGSGSSSEAIANRIALIKSQLETTSDPDR 358
QY 358 FDRKLOERLAKLAGVAVIKVGAFTETALKEKMLRIEDALNATRAVEGSIYAGGTAITLV 417
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 358 FDRKLOERLAKLAGVAVIKVGAFTETALKEKMLRIEDALNATRAVEGSIYAGGTAITLV 418
QY 418 ITVIEKVALELEDGATGRNIVLRALPEPVROIALNAGVSVYIDLKNSPAGTGPNATG 477
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 418 ITVIEKVALELEDGATGRNIVLRALPEPVROIALNAGVSVYIDLKNSPAGTGPNATG 478
QY 478 ATGEVDMITGTIDIPVKVTRSAALONAAVASLITTEVAANKPEPATPAMPAGMDPGM 537
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 478 ATGEVDMITGTIDIPVKVTRSAALONAAVASLITTEVAANKPEPATPAMPAGMDPGM 536
QY 538 GNM 540
   |||
DB 538 GNM 539

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Search completed: April 8, 2003, 14:25:19  
Job time : 23 secs